RAW SEQUENCE LISTING   DATE: 08/09/2004
PATENT APPLICATION: **US/10/679,580A**   TIME: 10:30:59

Input Set : **A:\224378.ST25.txt**
Output Set: **N:\CRF4\08092004\J679580A.raw**

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 3 <110> APPLICANT: Usha KASID
 4         Deepak KUMAR
 5         Irman AHMAD
 7 <120> TITLE OF INVENTION: GENE SCC-112 AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
 9 <130> FILE REFERENCE: 224378
W--> 10 <140> CURRENT APPLICATION NUMBER: US/10/679,580A
11 <141> CURRENT FILING DATE: 2003-10-06
12 <150> PRIOR APPLICATION NUMBER: PCT/US02/10850
13 <151> PRIOR FILING DATE: 2002-04-08
15 <150> PRIOR APPLICATION NUMBER: 60/281,780
16 <151> PRIOR FILING DATE: 2001-04-06
18 <160> NUMBER OF SEQ ID NOS: 3
20 <170> SOFTWARE: PatentIn Ver. 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 6744
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
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28 <221> NAME/KEY: CDS
29 <222> LOCATION: (232)..(4122)
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36 gcgtgcgggc gggccgcggg ggtcccggac ggacacaagc gcacacactc ccggaagatc 180
38 gcttaccctc cggggggtaaa agagatcacc gacaagatca ccacggacga g atg atc 237
39                                                          Met Ile
40                                                           1
42 aaa cgc ctg aag atg gta gtg aaa acc ttt atg gat atg gat cag gac 285
43 Lys Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp
44          5                    10                    15
46 tca gaa gat gaa aaa cag cag tat ctc cca cta gcc ttg cat ctt gca 333
47 Ser Glu Asp Glu Lys Gln Gln Tyr Leu Pro Leu Ala Leu His Leu Ala
48       20                    25                    30
50 tct gaa ttc ttc ctc agg aac ccc aat aaa gat gtg cgt ctc ctt gta 381
51 Ser Glu Phe Phe Leu Arg Asn Pro Asn Lys Asp Val Arg Leu Leu Val
52    35                    40                    45                50
54 gca tgt tgt ttg gct gat atc ttt cgt atc tat gcc cca gaa gct cca 429
55 Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro
56                55                    60                    65
58 tat act tcc cat gat aaa ctt aag gac ata ttt ttg ttt att acc aga 477
59 Tyr Thr Ser His Asp Lys Leu Lys Asp Ile Phe Leu Phe Ile Thr Arg
60             70                    75                    80
62 caa tta aaa ggt ttg gag gat aca aag agt cca cag ttt aat aga tac 525
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63 Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg Tyr
64         85                  90                  95
66 ttt tat tta tta gag aat tta gct tgg gtt aaa tca tat aac atc tgc    573
67 Phe Tyr Leu Leu Glu Asn Leu Ala Trp Val Lys Ser Tyr Asn Ile Cys
68         100                 105                 110
70 ttt gaa ttg gaa gat tgc aat gaa att ttt att cag ctt ttt aga act    621
71 Phe Glu Leu Glu Asp Cys Asn Glu Ile Phe Ile Gln Leu Phe Arg Thr
72 115                 120                 125                 130
74 ctc ttc tca gtg atc aac aat agc cac aat aag aag gta caa atg cac    669
75 Leu Phe Ser Val Ile Asn Asn Ser His Asn Lys Lys Val Gln Met His
76         135                 140                 145
78 atg cta gat ttg atg agt tct atc atc atg gaa ggt gat gga gtt act    717
79 Met Leu Asp Leu Met Ser Ser Ile Ile Met Glu Gly Asp Gly Val Thr
80         150                 155                 160
82 caa gaa tta ttg ggc tcc att ctt att aac ctc att cct gca cat aag    765
83 Gln Glu Leu Leu Gly Ser Ile Leu Ile Asn Leu Ile Pro Ala His Lys
84         165                 170                 175
86 aac tta aat aaa cag tcc ttt gac ctt gca aaa gtg cta ttg aaa aga    813
87 Asn Leu Asn Lys Gln Ser Phe Asp Leu Ala Lys Val Leu Leu Lys Arg
88         180                 185                 190
90 aca gtc cag act att gag gca tgc att gcc aat ttt ttc aat caa gtc    861
91 Thr Val Gln Thr Ile Glu Ala Cys Ile Ala Asn Phe Phe Asn Gln Val
92 195                 200                 205                 210
94 ctg gtg ctg gga aga tca tca gta agt gat ttg tca gaa cat gta ttt    909
95 Leu Val Leu Gly Arg Ser Ser Val Ser Asp Leu Ser Glu His Val Phe
96         215                 220                 225
98 gat ctg att cag gaa ctt ttt gct ata gat cct cat tta tta tta tcc    957
99 Asp Leu Ile Gln Glu Leu Phe Ala Ile Asp Pro His Leu Leu Leu Ser
100        230                 235                 240
102 gtc atg cca cag ctt gaa ttc aaa cta aag agc aat gat gga gaa gag  1005
103 Val Met Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Gly Glu Glu
104         245                 250                 255
106 cga tta gct gtt gtt cga ctt cta gct aaa ttg ttt ggc tcc aaa gat  1053
107 Arg Leu Ala Val Val Arg Leu Leu Ala Lys Leu Phe Gly Ser Lys Asp
108        260                 265                 270
110 tct gat ttg gca aca cag aat cgt cct ctt tgg caa tgt ttt ctt gga  1101
111 Ser Asp Leu Ala Thr Gln Asn Arg Pro Leu Trp Gln Cys Phe Leu Gly
112 275                 280                 285                 290
114 cga ttt aat gat att cat gtt cct gtg aga tta gaa agt gtg aaa ttt  1149
115 Arg Phe Asn Asp Ile His Val Pro Val Arg Leu Glu Ser Val Lys Phe
116        295                 300                 305
118 gcc agt cat tgt tta atg aat cac cca gat tta gcg aag gat ctc aca  1197
119 Ala Ser His Cys Leu Met Asn His Pro Asp Leu Ala Lys Asp Leu Thr
120        310                 315                 320
122 gaa tat tta aag gtt aga tca cat gat cca gaa gaa gct att cgt cat  1245
123 Glu Tyr Leu Lys Val Arg Ser His Asp Pro Glu Glu Ala Ile Arg His
124        325                 330                 335
126 gat gtc att gtt act ata ata aca gct gcc aag agg gac ctg gcc tta  1293
127 Asp Val Ile Val Thr Ile Ile Thr Ala Ala Lys Arg Asp Leu Ala Leu
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128      340                  345                  350
130 gta aat gat cag ctg ctt ggc ttt gta agg gaa aga aca ctg gat aaa    1341
131 Val Asn Asp Gln Leu Leu Gly Phe Val Arg Glu Arg Thr Leu Asp Lys
132 355              360                  365                  370
134 cgg tgg cga gta aga aaa gaa gct atg atg ggt ctg gct cag ctt tat    1389
135 Arg Trp Arg Val Arg Lys Glu Ala Met Met Gly Leu Ala Gln Leu Tyr
136              375                  380                  385
138 aag aaa tac tgt ctt cat ggt gaa gca gga aag gaa gct gca gag aaa    1437
139 Lys Lys Tyr Cys Leu His Gly Glu Ala Gly Lys Glu Ala Ala Glu Lys
140              390                  395                  400
142 gtc agc tgg ata aag gac aaa ctt ctg cat att tat tat cag aac agc    1485
143 Val Ser Trp Ile Lys Asp Lys Leu Leu His Ile Tyr Tyr Gln Asn Ser
144              405                  410                  415
146 att gac gac aaa ctg ttg gta gag aaa atc ttt gct cag tat ctt gtc    1533
147 Ile Asp Asp Lys Leu Leu Val Glu Lys Ile Phe Ala Gln Tyr Leu Val
148      420                  425                  430
150 ccc cac aac ctg gaa aca gaa gag aga atg aaa tgc tta tat tac tta    1581
151 Pro His Asn Leu Glu Thr Glu Glu Arg Met Lys Cys Leu Tyr Tyr Leu
152 435              440                  445                  450
154 tat gct agt ttg gat cca aat gct gta aaa gct ctc aac gaa atg tgg    1629
155 Tyr Ala Ser Leu Asp Pro Asn Ala Val Lys Ala Leu Asn Glu Met Trp
156              455                  460                  465
158 aag tgt cag aac atg ctt cgg agc cat gta cgc gaa cta ttg gat ttg    1677
159 Lys Cys Gln Asn Met Leu Arg Ser His Val Arg Glu Leu Leu Asp Leu
160              470                  475                  480
162 cac aag cag cct aca tca gag gct aac tgt tct gcc atg ttt gga aaa    1725
163 His Lys Gln Pro Thr Ser Glu Ala Asn Cys Ser Ala Met Phe Gly Lys
164              485                  490                  495
166 ctg atg acc ata gca aag aat ttg cct gac ccc ggg aaa gca caa gat    1773
167 Leu Met Thr Ile Ala Lys Asn Leu Pro Asp Pro Gly Lys Ala Gln Asp
168      500                  505                  510
170 ttt gtg aag aaa ttt aac cag gtt ctc ggc gat gat gag aaa ctt cgg    1821
171 Phe Val Lys Lys Phe Asn Gln Val Leu Gly Asp Asp Glu Lys Leu Arg
172 515              520                  525                  530
174 tct cag ttg gag tta tta att agc cca acc tgt tct tgc aaa caa gca    1869
175 Ser Gln Leu Glu Leu Leu Ile Ser Pro Thr Cys Ser Cys Lys Gln Ala
176              535                  540                  545
178 gat att tgt gtg aga gaa ata gcc cgg aaa ctt gca aat cct aag caa    1917
179 Asp Ile Cys Val Arg Glu Ile Ala Arg Lys Leu Ala Asn Pro Lys Gln
180              550                  555                  560
182 cca aca aat cct ttt cta gag atg gtc aaa ttt ctg ttg gaa aga atc    1965
183 Pro Thr Asn Pro Phe Leu Glu Met Val Lys Phe Leu Leu Glu Arg Ile
184              565                  570                  575
186 gca cct gtg cac att gat tca gaa gcc ata agt gca cta gtg aaa ttg    2013
187 Ala Pro Val His Ile Asp Ser Glu Ala Ile Ser Ala Leu Val Lys Leu
188      580                  585                  590
190 atg aat aag tca ata gag ggg aca gca gat gat gaa gag gag ggt gta    2061
191 Met Asn Lys Ser Ile Glu Gly Thr Ala Asp Asp Glu Glu Glu Gly Val
192 595              600                  605                  610
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194 agt cca gat aca gct atc cgt tca gga ctt gaa ctt ctt aag gtt ctg    2109
195 Ser Pro Asp Thr Ala Ile Arg Ser Gly Leu Glu Leu Leu Lys Val Leu
196             615              ·           620               625
198 tct ttt aca cat cct acc tcg ttc cac tct gca gag aca tat gag tcc    2157
199 Ser Phe Thr His Pro Thr Ser Phe His Ser Ala Glu Thr Tyr Glu Ser
200             630               . 635                   640
202 ttg tta cag tgc cta aga atg gag gat gac aag gta gca gaa gct gct    2205
203 Leu Leu Gln Cys Leu Arg Met Glu Asp Asp Lys Val Ala Glu Ala Ala
204             645                650                   655
206 att caa att ttt aga aat aca ggt cac aaa ata gaa aca gac ctt ccc    2253
207 Ile Gln Ile Phe Arg Asn Thr Gly His Lys Ile Glu Thr Asp Leu Pro
208       660                665                   670
210 cag ata cga tcg acc tta att ccc att tta cat caa aaa gca aag agg    2301
211 Gln Ile Arg Ser Thr Leu Ile Pro Ile Leu His Gln Lys Ala Lys Arg
212 675                 680                 685               690
214 ggt act cca cac caa gca aaa cag gct gtg cac tgt ata cac gcc ata    2349
215 Gly Thr Pro His Gln Ala Lys Gln Ala Val His Cys Ile His Ala Ile
216                 695                 700               . 705
218 ttc aca aat aaa gaa gtc cag ctt gca cag att ttt gag cca ctc agt    2397
219 Phe Thr Asn Lys Glu Val Gln Leu Ala Gln Ile Phe Glu Pro Leu Ser
220             710                 715                   720
222 agg agt ctg aat gct gat gtg cca gaa caa ctt ata act cca tta gtt    2445
223 Arg Ser Leu Asn Ala Asp Val Pro Glu Gln Leu Ile Thr Pro Leu Val
224             725                 730                   735
226 tca ttg ggc cac att tct atg tta gca cca gat cag ttt gct tcc cca    2493
227 Ser Leu Gly His Ile Ser Met Leu Ala Pro Asp Gln Phe Ala Ser Pro
228       740                 745                   750
230 atg aaa tct gta gta gca aat ttt att gtg aaa gat ctg cta atg aat    2541
231 Met Lys Ser Val Val Ala Asn Phe Ile Val Lys Asp Leu Leu Met Asn
232 755                 760                 765               770
234 gac agg tca aca ggt gaa aag aat gga aaa ctg tgg tct cca gat gaa    2589
235 Asp Arg Ser Thr Gly Glu Lys Asn Gly Lys Leu Trp Ser Pro Asp Glu
236             775                 780                   785
238 gag gtt tcc cct gaa gta cta gca aag gta cag gca att aaa ctt ctg    2637
239 Glu Val Ser Pro Glu Val Leu Ala Lys Val Gln Ala Ile Lys Leu Leu
240             790                 795                   800
242 gta agg tgg ctg ttg ggt atg aaa aac aac cag tct aaa tct gcc aat    2685
243 Val Arg Trp Leu Leu Gly Met Lys Asn Asn Gln Ser Lys Ser Ala Asn
244             805                 810                   815
246 tca acc ctt cgg tta tta tca gcg atg ttg gtt agt gag ggt gac ctg    2733
247 Ser Thr Leu Arg Leu Leu Ser Ala Met Leu Val Ser Glu Gly Asp Leu
248       820                 825                   830
250 aca gag caa aag agg atc agt aaa tct gat atg tct cgc ttg cga tta    2781
251 Thr Glu Gln Lys Arg Ile Ser Lys Ser Asp Met Ser Arg Leu Arg Leu
252 835                 840                 845               850
254 gct gct ggt agt gcc ata atg aag ctt gct cag gaa cct tgt tac cat    2829
255 Ala Ala Gly Ser Ala Ile Met Lys Leu Ala Gln Glu Pro Cys Tyr His
256             855                 860                   865
258 gaa att att acc cca gaa cag ttt cag ctc tgt gca ctt gtt att aat    2877
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259 Glu Ile Ile Thr Pro Glu Gln Phe Gln Leu Cys Ala Leu Val Ile Asn
260               870             875             880
262 gat gag tgt tac caa gta agg cag ata ttt gct cag aag ctg cat aag   2925
263 Asp Glu Cys Tyr Gln Val Arg Gln Ile Phe Ala Gln Lys Leu His Lys
264       885             890             895
266 gca ctt gtg aag tta ctg ctc cca ttg gag tat atg gcg atc ttt gcc   2973
267 Ala Leu Val Lys Leu Leu Leu Pro Leu Glu Tyr Met Ala Ile Phe Ala
268       900             905             910
270 ttg tgt gcc aaa gat cct gtg aag gag aga aga gca cac gca cga caa   3021
271 Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg Gln
272 915             920             925             930
274 tgt tta ctg aaa aat atc agt ata cgc agg gaa tac att aag cag aat   3069
275 Cys Leu Leu Lys Asn Ile Ser Ile Arg Arg Glu Tyr Ile Lys Gln Asn
276               935             940             945
278 cct atg gct act gag aaa tta tta tca ctg ttg cct gaa tat gta gtt   3117
279 Pro Met Ala Thr Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val Val
280               950             955             960
282 cca tac atg att cac ctg cta gcc cat gat cca gat ttt aca aga tca   3165
283 Pro Tyr Met Ile His Leu Leu Ala His Asp Pro Asp Phe Thr Arg Ser
284       965             970             975
286 caa gat gtt gat cag ctt cgt gat atc aaa gag tgc cta tgg ttc atg   3213
287 Gln Asp Val Asp Gln Leu Arg Asp Ile Lys Glu Cys Leu Trp Phe Met
288       980             985             990
290 ctt gaa gtt tta atg aca aag aat gaa aac aat agc cat gcc ttt atg   3261
291 Leu Glu Val Leu Met Thr Lys Asn Glu Asn Asn Ser His Ala Phe Met
292 995             1000            1005            1010
294 aag aag atg gca gag aac atc aag tta acc aga gat gcc cag tct cca   3309
295 Lys Lys Met Ala Glu Asn Ile Lys Leu Thr Arg Asp Ala Gln Ser Pro
296             1015            1020            1025
298 gat gaa tcc aag aca aat gaa aaa ctg tat aca gta tgt gat gtg gct   3357
299 Asp Glu Ser Lys Thr Asn Glu Lys Leu Tyr Thr Val Cys Asp Val Ala
300             1030            1035            1040
302 ctc tgt gtt ata aat agt aaa agt gct ttg tgc aat gca gat tca cca   3405
303 Leu Cys Val Ile Asn Ser Lys Ser Ala Leu Cys Asn Ala Asp Ser Pro
304       1045            1050            1055
306 aag gac cca gtc ctc cca atg aaa ttt ttt aca caa cct gaa aag gac   3453
307 Lys Asp Pro Val Leu Pro Met Lys Phe Phe Thr Gln Pro Glu Lys Asp
308     1060            1065            1070
310 ttc tgt aac gat aag agt tat att tca gaa gag aca aga gta ctt ctg   3501
311 Phe Cys Asn Asp Lys Ser Tyr Ile Ser Glu Glu Thr Arg Val Leu Leu
312 1075            1080            1085            1090
314 tta aca gga aag cca aag cct gct gga gta cta ggt gca gta aat aag   3549
315 Leu Thr Gly Lys Pro Lys Pro Ala Gly Val Leu Gly Ala Val Asn Lys
316             1095            1100            1105
318 cct tta tca gca acg gga agg aaa ccc tat gtt aga agc act ggc act   3597
319 Pro Leu Ser Ala Thr Gly Arg Lys Pro Tyr Val Arg Ser Thr Gly Thr
320             1110            1115            1120
322 gag act gga agc aat att aat gta aat tca gag ctg aac cct tca acc   3645
323 Glu Thr Gly Ser Asn Ile Asn Val Asn Ser Glu Leu Asn Pro Ser Thr
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/09/2004
PATENT APPLICATION: US/10/679,580A   TIME: 10:31:00

Input Set : **A:\224378.ST25.txt**
Output Set: **N:\CRF4\08092004\J679580A.raw**

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3

VERIFICATION SUMMARY   DATE: 08/09/2004
PATENT APPLICATION: **US/10/679,580A**   TIME: 10:31:00

Input Set : **A:\224378.ST25.txt**
Output Set: **N:\CRF4\08092004\J679580A.raw**

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